



1

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANTS: Björck, Lars  
Sjöbring, Ulf
- (ii) TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
- (iii) NUMBER OF SEQUENCES: 15
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Seed IP Law Group
  - (B) STREET: 701 Fifth Avenue Suite 6300
  - (C) CITY: Seattle
  - (D) STATE: Washington
  - (E) COUNTRY: USA
  - (F) ZIP: 98104-7092
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/325,278
  - (B) FILING DATE: 26-OCT-1994
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Potter, Jane E. R.
  - (B) REGISTRATION NUMBER: 33,332
  - (C) REFERENCE/DOCKET NUMBER: 100084.402
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (206) 622-4900
  - (B) TELEFAX: (206) 682-6031

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 305 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Escherichia coli LE392/pHDL, DSM 7054

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ala Val Glu Asn Lys Glu Glu Thr Pro Glu Thr Pro Glu Thr Asp Ser  
1 5 10 15

Glu Glu Glu Val Thr Ile Lys Ala Asn Leu Ile Phe Ala Asn Gly Ser  
20 25 30

Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Lys Ala Thr Ser Glu  
35 40 45

Ala Tyr Ala Tyr Ala Asp Thr Leu Lys Lys Asp Asn Gly Glu Tyr Thr  
50 55 60

Val Asp Val Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly  
65 70 75 80

Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala  
85 90 95

Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly  
100 105 110

Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Ala Leu  
115 120 125

Lys Lys Asp Asn Gly Glu Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr  
130 135 140

Thr Leu Asn Ile Lys Phe Ala Gly Lys Glu Lys Thr Pro Glu Glu Pro  
145 150 155 160

Lys Glu Glu Val Thr Ile Lys Ala Asn Leu Ile Tyr Ala Asp Gly Lys  
165 170 175

Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Glu Ala Thr Ala Glu  
180 185 190

Ala Tyr Arg Tyr Ala Asp Leu Leu Ala Lys Glu Asn Gly Lys Tyr Thr  
195 200 205

Val Asp Val Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly  
210 215 220

Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala  
225 230 235 240

Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly  
245 250 255

Thr Phe Ala Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu Leu  
260 265 270

Ala Lys Glu Asn Gly Lys Tyr Thr Ala Asp Leu Glu Asp Gly Gly Tyr  
275 280 285

Thr Ile Asn Ile Arg Phe Ala Gly Lys Lys Val Asp Glu Lys Pro Glu  
 290                            295                            300

Glu  
 305

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 921 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Escherichia coli LE392/pHDL, DSM 7054

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GCGGTAGAAA ATAAAGAAGA AACACCAGAA ACACCAAGAAA	60
CTGATTCAAGA AGAAGAAGTA	
ACAATCAAAG CTAACCTAAT CTTTGCAAAT GGAAGCACAC	120
AAACTGCAGA ATTCAAAGGA	
ACATTTGAAA AAGCAACATC AGAAGCTTAT GCGTATGCAG	180
ATACCTTGAA GAAAGACAAT	
GGAGAAATATA CTGTAGATGT TGCAGATAAA GGTTTACATT	240
TAAATATTAA ATTTGCTGGA	
AAAGAAAAAA CACCAGAAGA ACCAAAAGAA GAAGTTACTA	300
TTAAAGCAAA CTTAATCTAT	
GCAGATGGAA AAACACAAAC AGCAGAACATT	360
AAAGGAACAT TTGAAGAAC AACAGCAGAA	
GCATACAGAT ATGCAGATGC ATTAAGAAG GACAATGGAG	420
AATATACAGT AGACGTTGCA	
GATAAAAGGTT ATACTTTAAA TATTAAATTG GCTGGAAAAG	480
AAAAAACACC AGAAGAACCA	
AAAGAAGAAG TTACTATTAA AGCAAACCTTA ATCTATGCAG	540
ATGGAAAAAC ACAAACAGCA	
GAATTCAAAG GAACATTGAGA AGAAGCAACA GCAGAACAT	600
ACAGATATGC TGACTTATT	
GCAAAAGAAA ATGGTAAATA TACAGTAGAC GTTGCAGATA	660
AAGGTTATAC TTTAAATATT	
AAATTTGCTG GAAAAGAAAA AACACCAGAA GAACCAAAAG	720
AAGAAGTTAC TATTAAAGCA	
AACTTAATCT ATGCAGATGG AAAAACTCAA ACAGCAGAGT	780
TCAAAGGAAC ATTTGCAGAA	
GCAACAGCAG AAGCATACAG ATACGCTGAC TTATTAGCAA	840
AAGAAAATGG TAAATATACA	
GCAGACTTAG AAGATGGTGG ATACACTATT AATATTAGAT	900
TTGCAGGTAAGA GAAAGTTGAC	
GAAAAACCAG AAGAATAATA A	921

## (2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 434 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Escherichia coli LE392/pHDLG; DSM 7055

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ala	Val	Glu	Asn	Lys	Glu	Glu	Thr	Pro	Glu	Thr	Pro	Glu	Thr	Asp	Ser
1				5				10				15			

Glu	Glu	Glu	Val	Thr	Ile	Lys	Ala	Asn	Leu	Ile	Phe	Ala	Asn	Gly	Ser
			20					25				30			

Thr	Gln	Thr	Ala	Glu	Phe	Lys	Gly	Thr	Phe	Glu	Lys	Ala	Thr	Ser	Glu
			35					40			45				

Ala	Tyr	Ala	Tyr	Ala	Asp	Thr	Leu	Lys	Lys	Asp	Asn	Gly	Glu	Tyr	Thr
				50			55			60					

Val	Asp	Val	Ala	Asp	Lys	Gly	Tyr	Thr	Leu	Asn	Ile	Lys	Phe	Ala	Gly
65					70				75			80			

Lys	Glu	Lys	Thr	Pro	Glu	Glu	Pro	Lys	Glu	Glu	Val	Thr	Ile	Lys	Ala
				85				90			95				

Asn	Leu	Ile	Tyr	Ala	Asp	Gly	Lys	Thr	Gln	Thr	Ala	Glu	Phe	Lys	Gly
					100			105			110				

Thr	Phe	Glu	Glu	Ala	Thr	Ala	Glu	Ala	Tyr	Arg	Tyr	Ala	Asp	Ala	Leu
	115					120				125					

Lys	Lys	Asp	Asn	Gly	Glu	Tyr	Thr	Val	Asp	Val	Ala	Asp	Lys	Gly	Tyr
130					135				140						

Thr	Leu	Asn	Ile	Lys	Phe	Ala	Gly	Lys	Glu	Lys	Thr	Pro	Glu	Glu	Pro
145					150				155		160				

Lys	Glu	Glu	Val	Thr	Ile	Lys	Ala	Asn	Leu	Ile	Tyr	Ala	Asp	Gly	Lys
				165					170		175				

Thr	Gln	Thr	Ala	Glu	Phe	Lys	Gly	Thr	Phe	Glu	Glu	Ala	Thr	Ala	Glu
					180			185			190				

Ala	Tyr	Arg	Tyr	Ala	Asp	Leu	Leu	Ala	Lys	Glu	Asn	Gly	Lys	Tyr	Thr
					195			200			205				

Val Asp Val Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly  
 210 215 220  
 Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala  
 225 230 235 240  
 Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly  
 245 250 255  
 Thr Phe Ala Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu Leu  
 260 265 270  
 Ala Lys Glu Asn Gly Lys Tyr Thr Ala Asp Leu Glu Asp Gly Gly Tyr  
 275 280 285  
 Thr Ile Asn Ile Arg Phe Ala Gly Lys Lys Val Asp Glu Lys Pro Glu  
 290 295 300  
 Glu Pro Met Asp Thr Tyr Lys Leu Ile Leu Asn Gly Lys Thr Leu Lys  
 305 310 315 320  
 Gly Glu Thr Thr Glu Ala Val Asp Ala Ala Thr Ala Glu Lys Val  
 325 330 335  
 Phe Lys Gln Tyr Ala Asn Asp Asn Gly Val Asp Gly Glu Trp Thr Tyr  
 340 345 350  
 Asp Asp Ala Thr Lys Thr Phe Thr Val Thr Glu Lys Pro Glu Val Ile  
 355 360 365  
 Asp Ala Ser Glu Leu Thr Pro Ala Val Thr Thr Tyr Lys Leu Val Ile  
 370 375 380  
 Asn Gly Lys Thr Leu Lys Gly Glu Thr Thr Lys Ala Val Asp Ala  
 385 390 395 400  
 Glu Thr Ala Glu Lys Ala Phe Lys Gln Tyr Ala Asn Asp Asn Gly Val  
 405 410 415  
 Asp Gly Val Trp Thr Tyr Asp Asp Ala Thr Lys Thr Phe Thr Val Thr  
 420 425 430  
 Glu Met

## (2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1308 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Escherichia coli L392/pHDLG, DSM 7055

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCGGTAGAAA ATAAAGAAGA AACACCAGAA ACACCAGAAA CTGATTAGA AGAAGAAGTA	60
ACAATCAAAG CTAACCTAAT CTTGCAAAT GGAAGCACAC AAACATGCAGA ATTCAAAGGA	120
ACATTTGAAA AAGAACATC AGAAGCTTAT GCGTATGCAG ATACTTGAA GAAAGACAAT	180
GGAGAATATA CTGTAGATGT TGCAAGATAAA GGTTATACCT TAAATATTAA ATTTGCTGGA	240
AAAGAAAAAA CACCAGAAGA ACCAAAAGAA GAAGTTACTA TTAAAGCAA CTTAATCTAT	300
GCAGATGGAA AAACACAAAC AGCAGAATTG AAAGGAACAT TTGAAGAAC AACAGCAGAA	360
GCATACAGAT ATGCAGATGC ATTAAAGAAG GACAATGGAG AATATACAGT AGACGTTGCA	420
GATAAAGGTT ATACTTTAAA TATTAAATTG GCTGGAAAAG AAAAACACCC AGAAGAACCA	480
AAAGAAGAAG TTACTATTAA AGCAAACCTTA ATCTATGCAG ATGGAAAAAC ACAAACAGCA	540
GAATTCAAAG GAACATTGAGA AGAAGCAACA GCAGAAGCAT ACAGATATGC TGACTTATTA	600
GCAAAAGAAA ATGGTAAATA TACAGTAGAC GTTGCAGATA AAGGTTATAC TTTAAATATT	660
AAATTTGCTG GAAAAGAAAA AACACCAGAA GAACCAAAAG AAGAAGTTAC TATTAAAGCA	720
AACTTAATCT ATGCAGATGG AAAACTCAA ACAGCAGAGT TCAAAGGAAC ATTTGCAGAA	780
GCAACAGCAG AAGCATACAG ATACGCTGAC TTATTAGCAA AAGAAAATGG TAAATATACA	840
GCAGACTTAG AAGATGGTGG ATACACTATT AATATTAGAT TTGCAGGTAA GAAAGTTGAC	900
GAAAAACCAG AAGAACCCAT GGACACTTAC AAATTAATCC TTAATGGTAA AACATTGAAA	960
GGCGAAACAA CTACTGAAGC TGTTGATGCT GCTACTGCAG AAAAGTCCTT CAAACAATAC	1020
GCTAACGACA ACGGTGTTGA CGGTGAATGG ACTTACGACG ATGCGACTAA GACCTTACA	1080
GTTACTGAAA AACCAGAAAGT GATCGATGCG TCTGAATTAA CACCAGCCGT GACAACCTAC	1140
AAACTTGTAA TTAATGGTAA AACATTGAAA GGCGAAACAA CTACTAAAGC AGTAGACGCA	1200
GAAACTGCAG AAAAGCCTT CAAACAATAC GCTAACGACA ACGGTGTTGA TGGTGTGTTGG	1260
ACTTATGATG ATGCGACTAA GACCTTACG GTAACGTAAA TGTAATAA	1308

## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1332 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(A) NAME/KEY: CDS  
 (B) LOCATION: 1..1329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AAC GGT GAT GGT AAT CCT AGG GAA GTT ATA GAA GAT CTT GCA GCA AAC	48
Asn Gly Asp Gly Asn Pro Arg Glu Val Ile Glu Asp Leu Ala Ala Asn	
1 5 10 15	
AAT CCC GCA ATA CAA AAT ATA CGT TTA CGT CAC GAA AAC AAG GAC TTA	96
Asn Pro Ala Ile Gln Asn Ile Arg Leu Arg His Glu Asn Lys Asp Leu	
20 25 30	
AAA GCG AGA TTA GAG AAT GCA ATG GAA GTT GCA GGA AGA GAT TTT AAG	144
Lys Ala Arg Leu Glu Asn Ala Met Glu Val Ala Gly Arg Asp Phe Lys	
35 40 45	
AGA GCT GAA GAA CTT GAA AAA GCA AAA CAA GCC TTA GAA GAC CAG CGT	192
Arg Ala Glu Glu Leu Glu Lys Ala Lys Gln Ala Leu Glu Asp Gln Arg	
50 55 60	
AAA GAT TTA GAA ACT AAA TTA AAA GAA CTA CAA CAA GAC TAT GAC TTA	240
Lys Asp Leu Glu Thr Lys Leu Lys Glu Leu Gln Gln Asp Tyr Asp Leu	
65 70 75 80	
GCA AAG GAA TCA ACA AGT TGG GAT AGA CAA AGA CTT GAA AAA GAG TTA	288
Ala Lys Glu Ser Thr Ser Trp Asp Arg Gln Arg Leu Glu Lys Glu Leu	
85 90 95	
GAA GAG AAA AAG GAA GCT CTT GAA TTA GCG ATA GAC CAG GCA AGT CGG	336
Glu Glu Lys Lys Glu Ala Leu Glu Leu Ala Ile Asp Gln Ala Ser Arg	
100 105 110	
GAC TAC CAT AGA GCT ACC GCT TTA GAA AAA GAG TTA GAA GAG AAA AAG	384
Asp Tyr His Arg Ala Thr Ala Leu Glu Lys Glu Leu Glu Lys Lys Lys	
115 120 125	
AAA GCT CTT GAA TTA GCG ATA GAC CAA GCG AGT CAG GAC TAT AAT AGA	432
Lys Ala Leu Glu Leu Ala Ile Asp Gln Ala Ser Gln Asp Tyr Asn Arg	
130 135 140	
GCT AAC GTC TTA GAA AAA GAG TTA GAA ACG ATT ACT AGA GAA CAA GAG	480
Ala Asn Val Leu Glu Lys Glu Leu Glu Thr Ile Thr Arg Glu Gln Glu	
145 150 155 160	
ATT AAT CGT AAT CTT TTA GGC AAT GCA AAA CTT GAA CTT GAT CAA CTT	528
Ile Asn Arg Asn Leu Leu Gly Asn Ala Lys Leu Glu Leu Asp Gln Leu	

165	170	175	
TCA TCT GAA AAA GAG CAG CTA ACG ATC GAA AAA GCA AAA CTT GAG GAA Ser Ser Glu Lys Glu Gln Leu Thr Ile Glu Lys Ala Lys Leu Glu Glu 180	185	190	576
GAA AAA CAA ATC TCA GAC GCA AGT CGT CAA AGC CTT CGT CGT GAC TTG Glu Lys Gln Ile Ser Asp Ala Ser Arg Gln Ser Leu Arg Arg Asp Leu 195	200	205	624
GAC GCA TCA CGT GAA GCT AAG AAA CAG GTT GAA AAA GAT TTA GCA AAC Asp Ala Ser Arg Glu Ala Lys Lys Gln Val Glu Lys Asp Leu Ala Asn 210	215	220	672
TTG ACT GCT GAA CTT GAT AAG GTT AAA GAA GAC AAA CAA ATC TCA GAC Leu Thr Ala Glu Leu Asp Lys Val Lys Glu Asp Lys Gln Ile Ser Asp 225	230	235	720
GCA AGC CGT CAA CGG CTT CGC CGT GAC TTG GAC GCA TCA CGT GAA GCT Ala Ser Arg Gln Arg Leu Arg Arg Asp Leu Asp Ala Ser Arg Glu Ala 245	250	255	768
AAG AAA CAG GTT GAA AAA GAT TTA GCA AAC TTG ACT GCT GAA CTT GAT Lys Lys Gln Val Glu Lys Asp Leu Ala Asn Leu Thr Ala Glu Leu Asp 260	265	270	816
AAG GTT AAA GAA GAA AAA CAA ATC TCA GAC GCA AGC CGT CAA CGG CTT Lys Val Lys Glu Glu Lys Gln Ile Ser Asp Ala Ser Arg Gln Arg Leu 275	280	285	864
CGC CGT GAC TTG GAC GCA TCA CGT GAA GCT AAG AAA CAA GTT GAA AAA Arg Arg Asp Leu Asp Ala Ser Arg Glu Ala Lys Lys Gln Val Glu Lys 290	295	300	912
GCT TTA GAA GAA GCA AAC AGC AAA TTA GCT GCT CTT GAA AAA CTT AAC Ala Leu Glu Ala Asn Ser Lys Leu Ala Ala Leu Glu Lys Leu Asn 305	310	315	960
AAA GAG CTT GAA GAA AGC AAG AAA TTA ACA GAA AAA GAA AAA GCT GAA Lys Glu Leu Glu Glu Ser Lys Lys Leu Thr Glu Lys Glu Lys Ala Glu 325	330	335	1008
CTA CAA GCA AAA CTT GAA GCA GAA GCA AAA GCA CTC AAA GAA CAA TTA Leu Gln Ala Lys Leu Glu Ala Glu Ala Lys Ala Leu Lys Glu Gln Leu 340	345	350	1056
GCG AAA CAA GCT GAA GAA CTC GCA AAA CTA AGA GCT GGA AAA GCA TCA Ala Lys Gln Ala Glu Glu Leu Ala Lys Leu Arg Ala Gly Lys Ala Ser 355	360	365	1104
GAC TCA CAA ACC CCT GAT ACA AAA CCA GGA AAC AAA GCT CTT CCA GGT Asp Ser Gln Thr Pro Asp Thr Lys Pro Gly Asn Lys Val Leu Pro Gly 370	375	380	1152
AAA GGT CAA GCA CCA CAA GCA GGT ACA AAA CCT AAC CAA AAC AAA GCA Lys Gly Gln Ala Pro Gln Ala Gly Thr Lys Pro Asn Gln Asn Lys Ala 385	390	395	1200
			400

CCA ATG AAG GAA ACT AAG AGA CAG TTA CCA TCA ACA GGT GAA ACA GCT Pro Met Lys Glu Thr Lys Arg Gln Leu Pro Ser Thr Gly Glu Thr Ala 405 410 415	1248
AAC CCA TTC TTC ACA GCG GCA CGC GTT ACT GTT ATG GCA ACA GCT GGA Asn Pro Phe Phe Thr Ala Ala Arg Val Thr Val Met Ala Thr Ala Gly 420 425 430	1296
GTA GCA GCA GTT GTA AAA CGC AAA GAA GAA AAC TAA Val Ala Ala Val Val Lys Arg Lys Glu Glu Asn 435 440	1332

## (2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 443 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Asn Gly Asp Gly Asn Pro Arg Glu Val Ile Glu Asp Leu Ala Ala Asn 1 5 10 15
Asn Pro Ala Ile Gln Asn Ile Arg Leu Arg His Glu Asn Lys Asp Leu 20 25 30
Lys Ala Arg Leu Glu Asn Ala Met Glu Val Ala Gly Arg Asp Phe Lys 35 40 45
Arg Ala Glu Glu Leu Glu Lys Ala Lys Gln Ala Leu Glu Asp Gln Arg 50 55 60
Lys Asp Leu Glu Thr Lys Leu Lys Glu Leu Gln Gln Asp Tyr Asp Leu 65 70 75 80
Ala Lys Glu Ser Thr Ser Trp Asp Arg Gln Arg Leu Glu Lys Glu Leu 85 90 95
Glu Glu Lys Lys Glu Ala Leu Glu Leu Ala Ile Asp Gln Ala Ser Arg 100 105 110
Asp Tyr His Arg Ala Thr Ala Leu Glu Lys Glu Leu Glu Lys Lys 115 120 125
Lys Ala Leu Glu Leu Ala Ile Asp Gln Ala Ser Gln Asp Tyr Asn Arg 130 135 140
Ala Asn Val Leu Glu Lys Glu Leu Glu Thr Ile Thr Arg Glu Gln Glu 145 150 155 160
Ile Asn Arg Asn Leu Leu Gly Asn Ala Lys Leu Glu Leu Asp Gln Leu 165 170 175

Ser Ser Glu Lys Glu Gln Leu Thr Ile Glu Lys Ala Lys Leu Glu Glu  
 180 185 190  
 Glu Lys Gln Ile Ser Asp Ala Ser Arg Gln Ser Leu Arg Arg Asp Leu  
 195 200 205  
 Asp Ala Ser Arg Glu Ala Lys Lys Gln Val Glu Lys Asp Leu Ala Asn  
 210 215 220  
 Leu Thr Ala Glu Leu Asp Lys Val Lys Glu Asp Lys Gln Ile Ser Asp  
 225 230 235 240  
 Ala Ser Arg Gln Arg Leu Arg Arg Asp Leu Asp Ala Ser Arg Glu Ala  
 245 250 255  
 Lys Lys Gln Val Glu Lys Asp Leu Ala Asn Leu Thr Ala Glu Leu Asp  
 260 265 270  
 Lys Val Lys Glu Glu Lys Gln Ile Ser Asp Ala Ser Arg Gln Arg Leu  
 275 280 285  
 Arg Arg Asp Leu Asp Ala Ser Arg Glu Ala Lys Lys Gln Val Glu Lys  
 290 295 300  
 Ala Leu Glu Glu Ala Asn Ser Lys Leu Ala Ala Leu Glu Lys Leu Asn  
 305 310 315 320  
 Lys Glu Leu Glu Glu Ser Lys Lys Leu Thr Glu Lys Glu Lys Ala Glu  
 325 330 335  
 Leu Gln Ala Lys Leu Glu Ala Glu Ala Lys Ala Leu Lys Glu Gln Leu  
 340 345 350  
 Ala Lys Gln Ala Glu Glu Leu Ala Lys Leu Arg Ala Gly Lys Ala Ser  
 355 360 365  
 Asp Ser Gln Thr Pro Asp Thr Lys Pro Gly Asn Lys Ala Val Pro Gly  
 370 375 380  
 Lys Gly Gln Ala Pro Gln Ala Gly Thr Lys Pro Asn Gln Asn Lys Ala  
 385 390 395 400  
 Pro Met Lys Glu Thr Lys Arg Gln Leu Pro Ser Thr Gly Glu Thr Ala  
 405 410 415  
 Asn Pro Phe Phe Thr Ala Ala Arg Val Thr Val Met Ala Thr Ala Gly  
 420 425 430  
 Val Ala Ala Val Val Lys Arg Lys Glu Glu Asn  
 435 440

## (2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 44 base pairs
  - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCTCAGGCAG CGCCGGTAGA AAATAAAGAA GAAACACCAG AAAC

44

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 9 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Val Glu Asn Lys Glu Glu Thr Pro Glu  
1 5

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 47 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CAGCAGCAGG ATTCTTATTA TTCTTCTGGT TTTTCGTCAA CTTTCTT

47

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 44 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CAGCAGCAGC CATGGGTTCT TCTGGTTTT CGTCAACTTT CTTA

44

## (2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGCCATGGAC ACTTACAAAT TAATCCTTAA TGGT

34

## (2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met	Asp	Thr	Tyr	Lys	Leu	Ile	Leu	Asn	Gly
1				5				10	

## (2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 42 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CAGGTCGACT TATTACATTT CAGTTACCGT AAAGGTCTTA GT

42

## (2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 152 base pairs
  - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AAGCTTAAGG AGGTTAACG ATGAAAAAAA CTGCTATCGC TATCGCTGTT GCTCTGGCTG	60
GTTCGCTAC TGTTGCTCAG GCGGCGCCGA GATCTAAACA GGAATTGAG CTCGGTACCC	120
GGGGATCCTC TAGAGCTGAC CTGCAGGCAT GC	152

## (2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4 amino acids
  - (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Ala Val Glu Asn  
1